

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

Source:

Date Processed by STIC:

10/600,070A
JFW/16
5-26-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chknote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - cPAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

BEST AVAILABLE COPY

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/600,070A

ATTN: NEW RULES CASES: PLEASE DISCARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was received in a word processor after creating it. Please adjust your right margin to .5; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino Numbering The numbering under each 5' amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(1) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(11) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(11) NUMBER OF SEQUENCES" response to include the skipped sequence(s).

8 Skipped Sequences (NEW RULES) Sequence(s) 8 missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

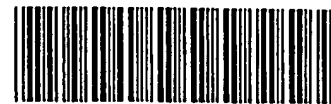
9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <21> Response Per 1.823 of Sequence Rules, the only valid <21> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <21> response is Unknown, Artificial Sequence.

11 Use of <210> Sequence(s) missing the <220>-<223> section and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <21> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules).

12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.



IFW16

RAW SEQUENCE LISTING

DATE: 05/26/2005

PATENT APPLICATION: US/10/600,070A

TIME: 12:34:01

Input Set : A:\08153.ST25.txt

Output Set: N:\CRF4\05262005\J600070A.raw

3 <110> APPLICANT: Osteryoung, Katherine W.
 4 Vitha, Stanislav
 5 Koksharova, Olga A.
 6 Gao, Hongo
 8 <120> TITLE OF INVENTION: Plastid Division and Related Genes and Proteins, and Methods
 of
 9 Use
 11 <130> FILE REFERENCE: MSU-08153
 13 <140> CURRENT APPLICATION NUMBER: 10/600,070A
 14 <141> CURRENT FILING DATE: 2003-06-20
 16 <160> NUMBER OF SEQ ID NOS: 208
 18 <170> SOFTWARE: PatentIn version 3.3

ERRORED SEQUENCES

811 <210> SEQ ID NO: 8
 812 <211> LENGTH: 0
 813 <212> TYPE: DNA
 814 <213> ORGANISM: Artificial Sequence
 816 <220> FEATURE:
 817 <223> OTHER INFORMATION: Synthetic
 820 <220> FEATURE:
 821 <221> NAME/KEY: misc_feature
 822 <223> OTHER INFORMATION: Intentionally omitted.
 824 <240> SEQUENCE: 8

E--> 824 8

Does Not Comply
 Corrected Diskette Needed
 (pg. 1-2)

See error explanation on page 2.

10/600,070A

Page 2

<210> 8
<211> 0
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc feature
<223> Intentionally omitted.

<400> 8
<210> 9
<211> 2406
<212> DNA
<213> Arabidopsis thaliana

<400> 9

insert
space

Whenever <221> is shown, <222> must be inserted.

delete

IF this sequence
was intentionally
skipped, pls
see item # 8
on error
summary sheet
for skipped
sequence
format.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VERIFICATION SUMMARY

DATE: 05/26/2005

PATENT APPLICATION: US/10/600,070A

TIME: 12:34:03

Input Set : A:\08153.ST25.txt

Output Set: N:\CRF4\05262005\J600070A.raw

L:824 M:301 E: (44) No Sequence Data was Shown, SEQ ID:8
L:7849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:132 after pos.:120
M:341 Repeated in SeqNo=132
L:8035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:140 after pos.:60
L:8134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:144 after pos.:120
M:341 Repeated in SeqNo=144
L:8195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:146 after pos.:0
M:341 Repeated in SeqNo=146
L:8235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:147 after pos.:0
M:341 Repeated in SeqNo=147
L:11295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174 after pos.:0
M:341 Repeated in SeqNo=174
L:11352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:175 after pos.:480
L:11514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:182 after pos.:0
L:11568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:184 after pos.:0
L:13263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:198 after pos.:600
L:13300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:199 after pos.:600
L:13368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:201 after pos.:600
L:13594 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:207 after pos.:0